

Sequences producing significant alignments:	Score (bits)	E Value	
gi 37182190 gb AY358534.1 Homo sapiens clone DNA76396 ESRM	4896	0.0	
<u>qi 21750076 dbj AK091656.1 </u> Homo sapiens cDNA FLJ34337 fis,	4869	0.0	
<u>qi 21750007 dbj AK091596.1 </u> Homo sapiens cDNA FLJ34277 fis, <u>qi 29126308 qb AC125494.2 </u> Homo sapiens 12 PAC RP4-761J14 (<u>4496</u> 3620	0.0	
<pre>gi 23273049 gb BC035736.1 Homo sapiens hypothetical protei</pre>	2444	0.0	
gi 31559779 ref NM 153685.2 Homo sapiens hypothetical prot	2444	0.0	
gi 16551656 dbj AK056295.1 Homo sapiens cDNA FLJ31733 fis,	2440	0.0	
gi[21.755198 dbj AK095854.1] Homo sapiens cDNA FLJ38535 fis,	2432	0.0	
<u>gi 21732368 emb AL831874.1 HSM803198</u> Homo sapiens mRNA; cDN	2018	0.0	
qi 14388568 dbj AB063097.1 Macaca fascicularis brain cDNAqi 9280141 dbj AB046043.1 Macaca fascicularis brain cDNA	<u>1951</u>	0.0	
,	<u> 1919</u>	0.0	******
gi 40787821 gb BC065170.1 Mus musculus RIKEN cDNA C5300280	829	0.0	
gi 26350162 dbj AK082984.1 Mus musculus 12 days embryo spi	781	0.0	
<u>qi 31342339 ref NM 175696.2 </u> Mus musculus RIKEN cDNA C53002	781	0.0	
<pre>gi 34858455 ref XM 232352.2 Rattus norvegicus similar to R</pre>	626	e-176	
<u>qi 33331884 gb AF540035.1 </u> Mus musculus brain protein 1 mRN	<u>569</u>	e-158	

<pre>gi 11527816 gb AF168681.1 Homo sapiens CRIM1 protein gene,</pre>	58	9e-0!	5
<u>qi 7839914 gb AC007378.4 AC007378</u> Homo sapiens BAC clone RP	58	9e-0!	
gi 33620859 gb AC102339.16 Mus musculus chromosome 18, clo		0.00	
gi 21211731 emb AL445426.20 Human DNA sequence from clone	52		
<u>gi 16554315 gb AC087892.16 </u> Homo sapiens 12q BAC RP11-3L23	<u> 52</u>	0.005	
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gi 15982602 gb AC093325.3 Homo sapiens BAC clone RP11-612J	<u>50</u>	0.021	
gi 41015639 gb AC121563.3 Mus musculus BAC clone RP23-198C	<u>50</u>	0.021	-
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<pre>qi 37591276 gb AC109805.8 Mus musculus chromosome 3, clone</pre>	48	0.085	·)
gi 35931852 qb AC102637.7 Mus musculus chromosome 6, clone	48	0.085)
qi 33859906 gb AC058788.89 Mus musculus clone rp23-284a9 m	48	0.085	
gi 21465364 gb AC011499.5 Homo sapiens chromosome 19 clone	48	0.085	
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gi 19034002 qb AC007002.3 Homo sapiens BAC clone RP11-493L	48	0.085	- 8 23
<u>gi 41016026 dbj AB114903.1 </u> Mus musculus Lmbr1 gene for LMB	<u>48</u>	0.085	
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<u>qi 16445088 gb AC012464.25 </u> Homo sapiens 12 BAC RP11-1060G2	46	0.33	
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$\underline{\text{gi}[20279493]\text{gb}[AC087465.5]}$ Homo sapiens chromosome 15, clon	46	0.33	
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<u>qi 18999500 qb BC024275.1 </u> Homo sapiens, Similar to hypothe	46	0.33	
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Alignments

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results of NDAMI

BLASTN 2.2.8 [Jan-05-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

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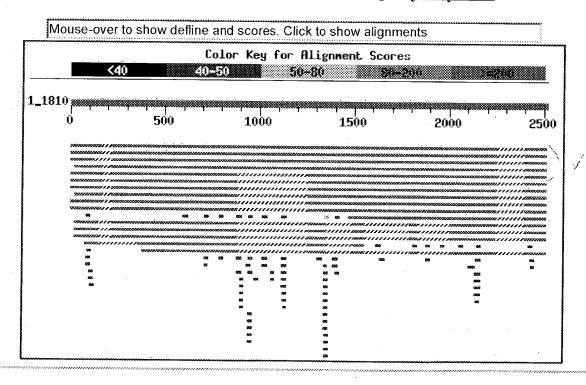
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Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)
2,092,142 sequences; 10,066,846,959 total letters

If you have any problems or questions with the results of this search please refer to the ${\tt BLAST\ FAQs}$

Taxonomy reports

Distribution of 156 Blast Hits on the Query Sequence



Score E

41 37182190 40 AY358554.1	Sequences producing significant alignments: SEQ ID NO:251	(bits)	Value	
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qi 22026895 ref NM 137508.2 Drosophila melanogaster CG5345 42 5.2 qi 24962936 qb AC125404.4 Mus musculus BAC clone RP23-10A1 42 5.2 qi 25141141 qb AC122233.4 Mus musculus BAC clone RP23-137D 42 5.2 qi 37700357 qb AC122158.17 Mus musculus clone ct7-43303 ma 42 5.2 qi 31795103 qb AC073585.8 Homo sapiens chromosome 10 clone 42 5.2 qi 21358710 qb AC095025.2 Sus scrofa clone RP44-93L12, com 42 5.2 qi 6563055 qb AF109422.1 Icterus laudabilis ATPase subunit 42 5.2 qi 6563054 qb AF109421.1 Icterus laudabilis ATPase subunit 42 5.2 qi 6563048 qb AF109420.1 Icterus laudabilis ATPase subunit 42 5.2 qi 6563048 qb AF109415.1 Icterus oberi ATPase subunit 8 (A 42 5.2 qi 6563047 qb AF109414.1 Icterus oberi ATPase subunit 8 (A 42 5.2 qi 6563046 qb AF109413.1 Icterus bonana ATPase subunit 8 (A 42 5.2				
gi 25141141 gb AC122233.4 Mus musculus BAC clone RP23-137D	gi 22026895 ref NM 137508.2 Drosophila melanogaster CG5345			
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gi 6563048 gb AF109415.1 Icterus oberi ATPase subunit 8 (A 42 5.2 gi 6563047 gb AF109414.1 Icterus oberi ATPase subunit 8 (A 42 5.2 gi 6563046 gb AF109413.1 Icterus bonana ATPase subunit 8 (42 5.2		42		
qi 6563047 gb AF109414.1 Icterus oberi ATPase subunit 8 (A 42 5.2 qi 6563046 gb AF109413.1 Icterus bonana ATPase subunit 8 (42 5.2	gi 6563048 gb AF109415.1 Icterus oberi ATPase subunit 8 (A			
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Alignments

Get selected sequences Select all Deselect all

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Score = 3998 bits (2017), Expect = 0.0
Identities = 2031/2035 (99%), Gaps = 3/2035 (0%)
Strand = Plus / Plus

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Strand = Plus / Plus

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Score = 3998 bits (2017), Expect = 0.0
Identities = 2031/2035 (99%), Gaps = 3/2035 (0%)
Strand = Plus / Plus
Query: 220 cgtcatgtgtgcgtgtgggagcgagcacctccaccaagccgatctcctcgggtcccaaga 279
        Sbjct: 161
        cqtcatqtgtgcgtgtgggagcgagcacctccaccaagccgatctcctcgggtcccaaga 220
        tcacgtcggcaagtcctgcctggcactgcaccccaagccaccccatcaggctttgaggag 339
Query: 280
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Sbjct: 221
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Query: 340
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Sbjct: 281
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Query: 460
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        Sbjct: 401
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Sbjct: 461
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Sbjct:	761		820
Query: Sbjct:		cggtgagggcaggggcaatgggatgggagggcaaagagggaaggcaacttaggtcttcag	
Query:	940	agctggggtggggtgccctctggatgggtagtgagggagg	999
Sbjct:	881		940
Query: Sbjct:		ccctggccctccaagggggctggaccagctcctctctgggaggcacccttcctt	
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		illilillililililililililililililililil	
-		tttgtcttgaacttccccttctattctggcctaccccttggttcctgactgtgccctttc	
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-		cctcttcctctcaggattcccctggtgaatctgtgatgcccccaatgttggggtgcagcc	
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_		gagctggggccacaggggctcctggctcctgccccttgcacaccacccggaacactcccc	
		gagctggggccacaggggctcctggctcctgccccttgcacaccacccggaacactcccc	

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Sbjct: 1361 agccccacgggcaatcctatctgctcgccctcctgcaggtgggggcctcacatatctgtg 1420
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       Sbjct: 1421 acttegggteeetgteeeeaceettgtgeacteacatgaaageettgeacaeteacetee 1480
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       Sbjct: 1541 agetgäeteteatgttetetegteteaeatttgeaeteteteteetteeaeattetgtget 1600
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Sbjct: 2021 cccttttgtcttgtctgtcctggctgtctgtgtgtgtgccattctctggacttcagagcc 2080
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```

```
Sbjct: 2081 ccctgagccagtcctcccttcccagcctccctttgggcctccctaactccacctaggctg 2140
Query: 2197 ccagggaccggagtcagctggttcaaggccatcgggagctctgcctccaagtcta 2251
        Sbict: 2141 ccaqqqaccqqaqtcagctggttcaaggccatcgggagctctgcctccaagtcta 2195
Score = 214 \text{ bits } (108), Expect = 6e-52
Identities = 125/130 (96\%), Gaps = 3/130 (2\%)
Strand = Plus / Plus
       cqccaaqcatqcaqtaaaqqctqc---tctqqqtcacaqctqaggaagacctcagacatg 57
Query: 1
       cgccaagcatgcagtaaaggctgaaaatctgggtcacagctgaggaagacctcagacatg 76
Sbjct: 17
Sbjet: 77 gagtecaggatgtggcetgegetgetgteceaectectecetetetggeeaetgetg 136
Query: 118 ttgctgcccc 127
       Sbjct: 137 ttgccgcccc 146
Score = 190 \text{ bits } (96), \text{ Expect = } 9e-45
Identities = 110/114 (96%), Gaps = 3/114 (2%)
Strand = Plus / Plus
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        Sbjct: 2405 cttgaattactgtgggatgtäagtttcaaaattttcaaataaagcctttgcaag 2458
🔲 >qi|29126308|gb|AC125494.2| 🗱 Homo sapiens 12 PAC RP4-761J14 (Roswell Park Cance
         Library) complete sequence
      Length = 143979
Score = 3128 bits (1578), Expect = 0.0
Identities = 1592/1596 (99%), Gaps = 3/1596 (0%)
Strand = Plus / Plus
         gctgggaccgcagacgcagacgcagaccctcagggcagcaaggtgccctgaggcagg 718
Query: 659
         Sbjet: 102763 getgggaccgcagecagaagegacgeagaeeetcagggcageaaggtgeeetgaggcagg 102822
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Query: Sbjct:		tcctggctcctgccccttgcacaccacccggaacactccccagccccacgggcaatccta	